



## AMENDMENTS TO THE SPECIFICATION

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Please replace the paragraph beginning at page 14, line 4, with the following rewritten paragraph:

--The alignment tools ALIGN (Myers and Miller, *CABIOS* 4:11-17, 1989) or LFASTA (Pearson and Lipman, *Proc. Natl. Acad. Sci., USA* 85:2444-2448, 1988) may be used to perform sequence comparisons (Internet Program © 1996, W. R. Pearson and the University of Virginia, "fasta20u63" version 2.0u63, release date December 1996). ALIGN compares entire sequences against one another, while LFASTA compares regions of local similarity. These alignment tools and their respective tutorials are available on the Internet at <http://biology.nesa.uiuc.edu>.--

Please replace the paragraph beginning at page 14, line 13, with the following rewritten paragraph:

--The NCBI Basic Local Alignment Search Tool (BLAST) (Altschul *et al.*, *J Mol Biol.* 1990 215:403-410, 1990) is available from several sources, including the National Center for Biotechnology Information (NCBI, Bethesda, MD) and on the Internet, for use in connection with the sequence analysis programs blastp, blastn, blastx, tblastn and tblastx. It can be accessed at the NCBI BLAST website <http://www.ncbi.nlm.nih.gov/BLAST/>. A description of how to determine sequence identity using this program is also available at the NCBI website BLAST tutorial [http://www.ncbi.nlm.nih.gov/BLAST/blast\\_help.html](http://www.ncbi.nlm.nih.gov/BLAST/blast_help.html).--

Please replace the paragraph beginning at page 14, line 33, with the following rewritten paragraph:

--When significantly less than the entire sequence is being compared for sequence identity, homologs will typically possess at least 80% sequence identity over short windows of 10-20 amino acids, and may possess sequence identities of at least 85%, at least 90%, at least 95%, or at least 99% depending on their similarity to the reference sequence. Sequence identity over such short windows can be determined using LFASTA; methods are described at <http://biology.nesa.uiuc.edu> on the Internet. One of skill in the art will appreciate that these sequence identity ranges are provided for guidance only; it is entirely possible that strongly

significant homologs could be obtained that fall outside of the ranges provided. The present invention provides not only the peptide homologs that are described above, but also nucleic acid molecules that encode such homologs.--

Please replace the paragraph beginning at page 19, line 19, with the following rewritten paragraph:

--In addition to these general guidelines, protein expression/purification kits are produced commercially. See, for instance, the QIAexpressQIAEXPRESS™ expression system from QIAGEN (Chatsworth, CA) and various expression systems provided by INVITROGEN (Carlsbad, CA). Depending on the details provided by the manufacturer, such kits can be used for production and purification of the disclosed bispecific fusion proteins.--

Please replace the paragraph beginning at page 19, line 34, with the following rewritten paragraph:

--Commercially produced protein expression/purification kits provide tailored protocols for the purification of proteins made using each system. See, for instance, the QIAexpressQIAEXPRESS™ expression system from QIAGEN (Chatsworth, CA) and various expression systems provided by INVITROGEN (Carlsbad, CA). Where a commercial kit is employed to produce a bispecific fusion protein, the manufacturer's purification protocol is a particularly disclosed protocol for purification of that protein. For instance, proteins expressed with an amino-terminal hexa-his tag can be purified by binding to nickel-nitrilotriacetic acid (Ni-NTA) metal affinity chromatography matrix (*The QIAexpressionist*, QIAGEN, 1997).--